CelD

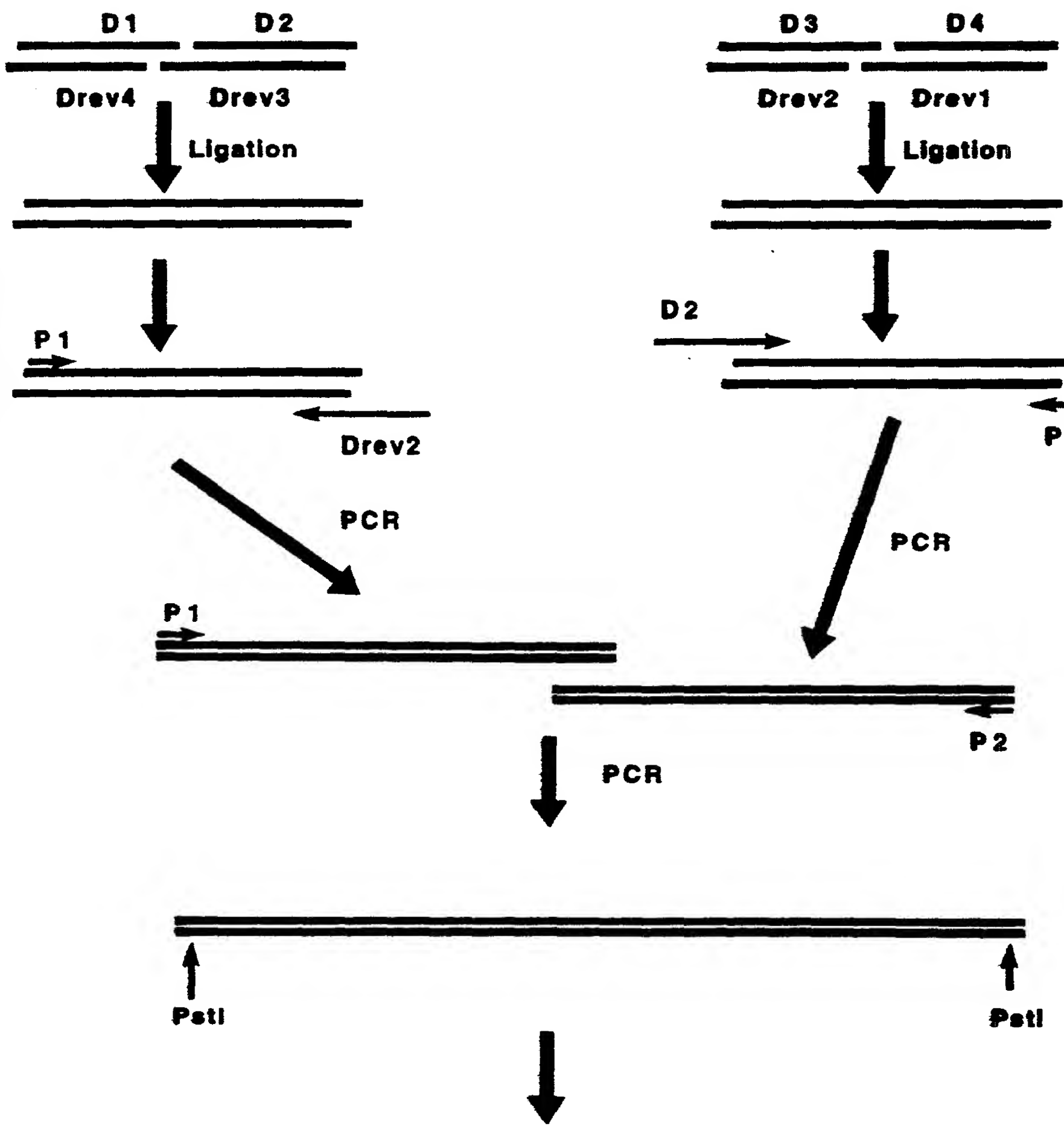
Val-Leu-Tyr-Gly-Asp-Val-Asn-AspAsp-Gly-Lys-Val-Asn-Ser-Thr-Asp-Leu-Thr-
Leu-Leu-Lys-Arg-Tyr-Val-Leu-Lys-Ala-Val-Ser-Thr-Leu-Pro-Ser-Ser-Lys-Ala-Glu-
Lys-Asn-Ala-Asp-Val-Asn-Arg-Asp-Gly-Arg-Val-Asn-Ser-Ser-Asp-Val-Thr-Ile-
Leu-Ser-Arg-Tyr-Leu-Ile-Arg-Val-Ile-Glu-Lys-Leu-Pro-Ile

CelS

Lys-Leu-Tyr-Gly-Asp-Val-Asn-Asp-Asp-Gly-Lys-Val-Asn-Ser-Thr-Asp-Ala-Val-
Ala-Leu-Lys-Arg-Tyr-Val-Leu-Arg-Ser-Gly-Ile-Ser-Ile-Asn-Thr-Asp-Asn-Ala-Asp-
Leu-Asn-Glu-Asp-Gly-Arg-Val-Asn-Ser-Thr-Asp-Leu-Gly-Ile-Leu-Lys-Arg-Tyr-Ile-
Leu-Lys-Glu-Ile-Asp-Thr-Leu-Pro-Tyr-Lys-Asn

**FIGURE 1**

**Assembly of DNA fragment encoding dockerin do**




Cloned in the PstI site of

pUC18 vector

FIGURE 2

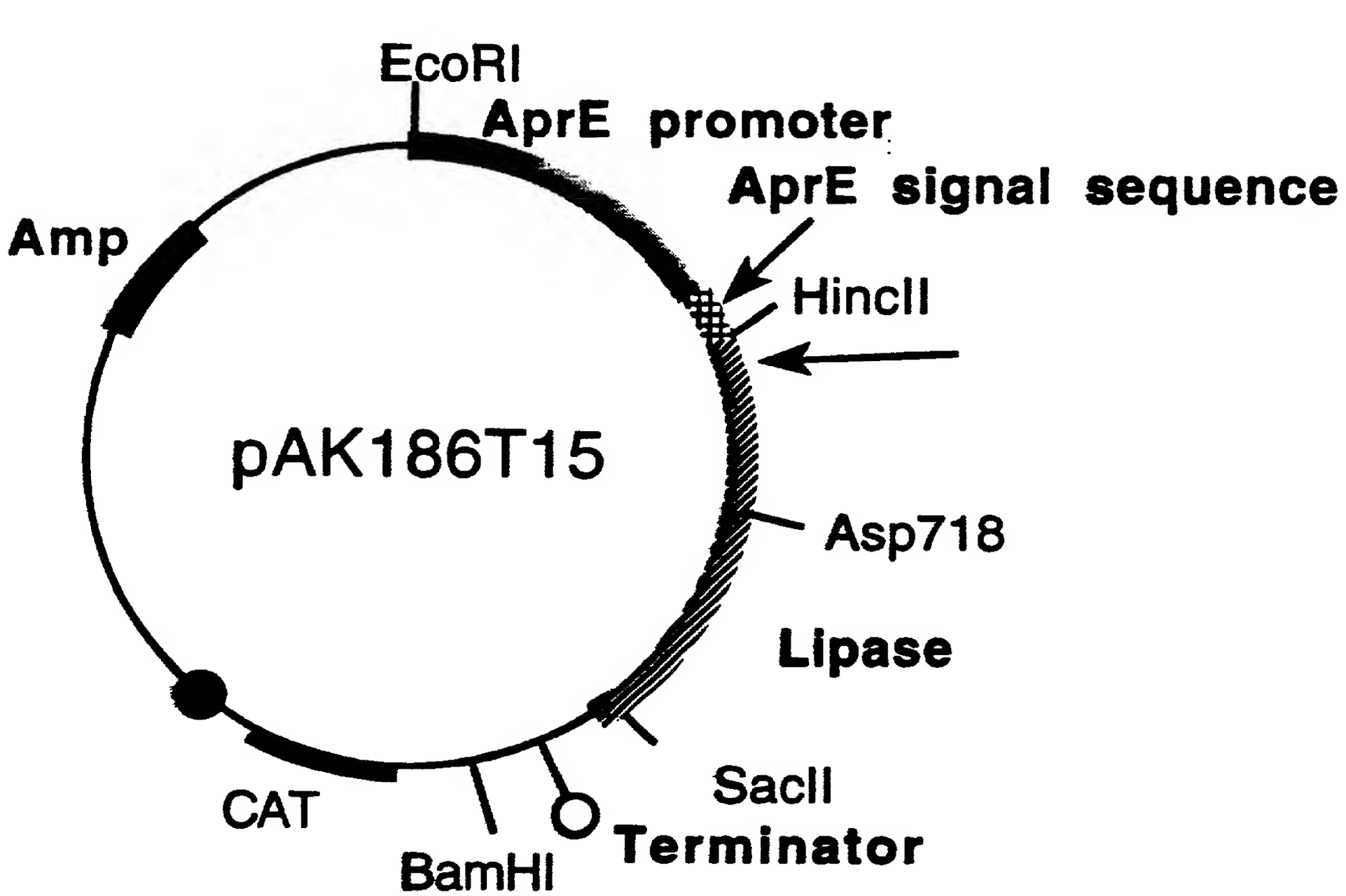

EcoRI
AprE promoter
AprE signal sequence
Amp
HincII
pAK186T15
Asp718
Lipase
SacII
Terminator
CAT
BamHI

FIGURE 3

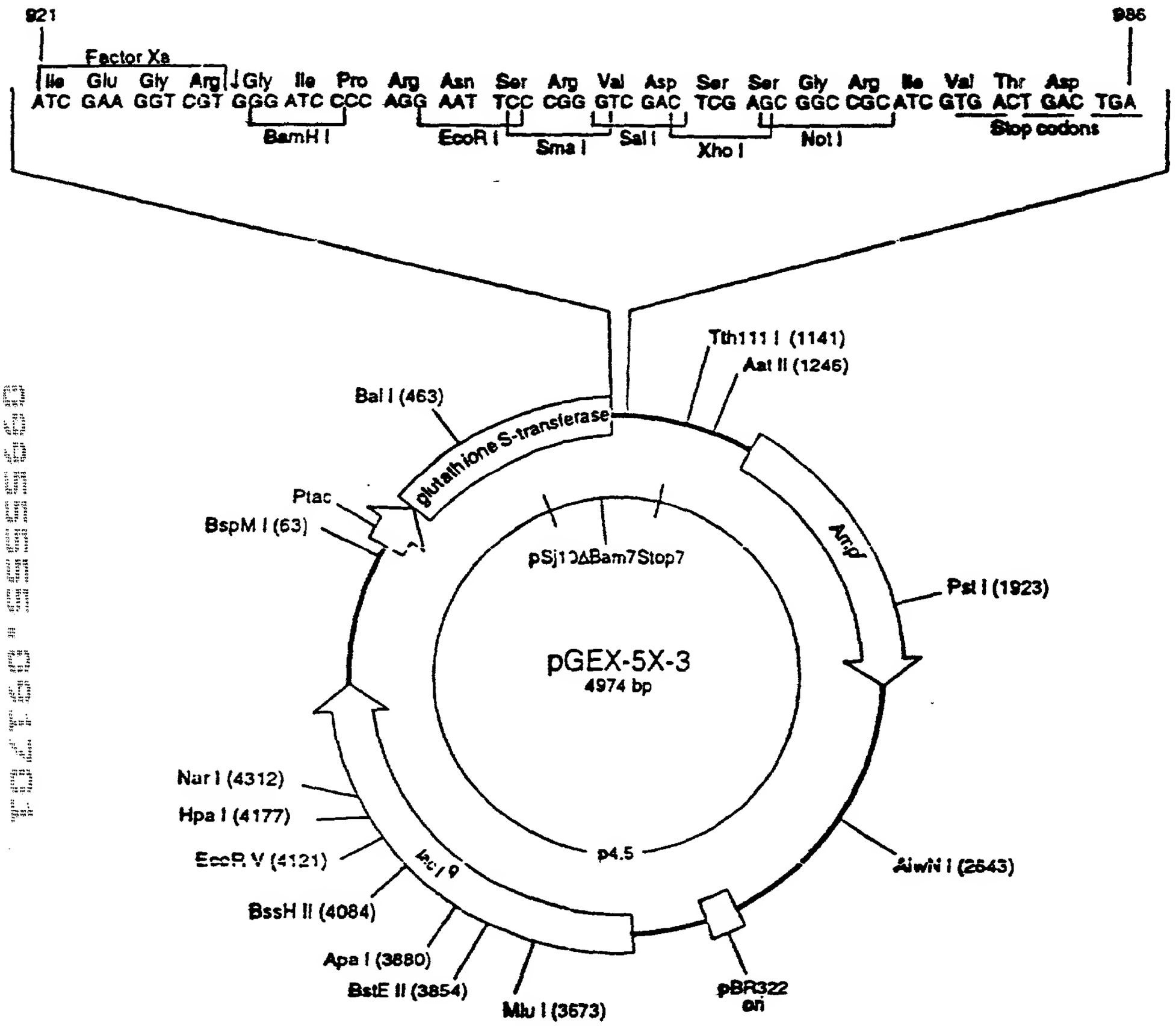
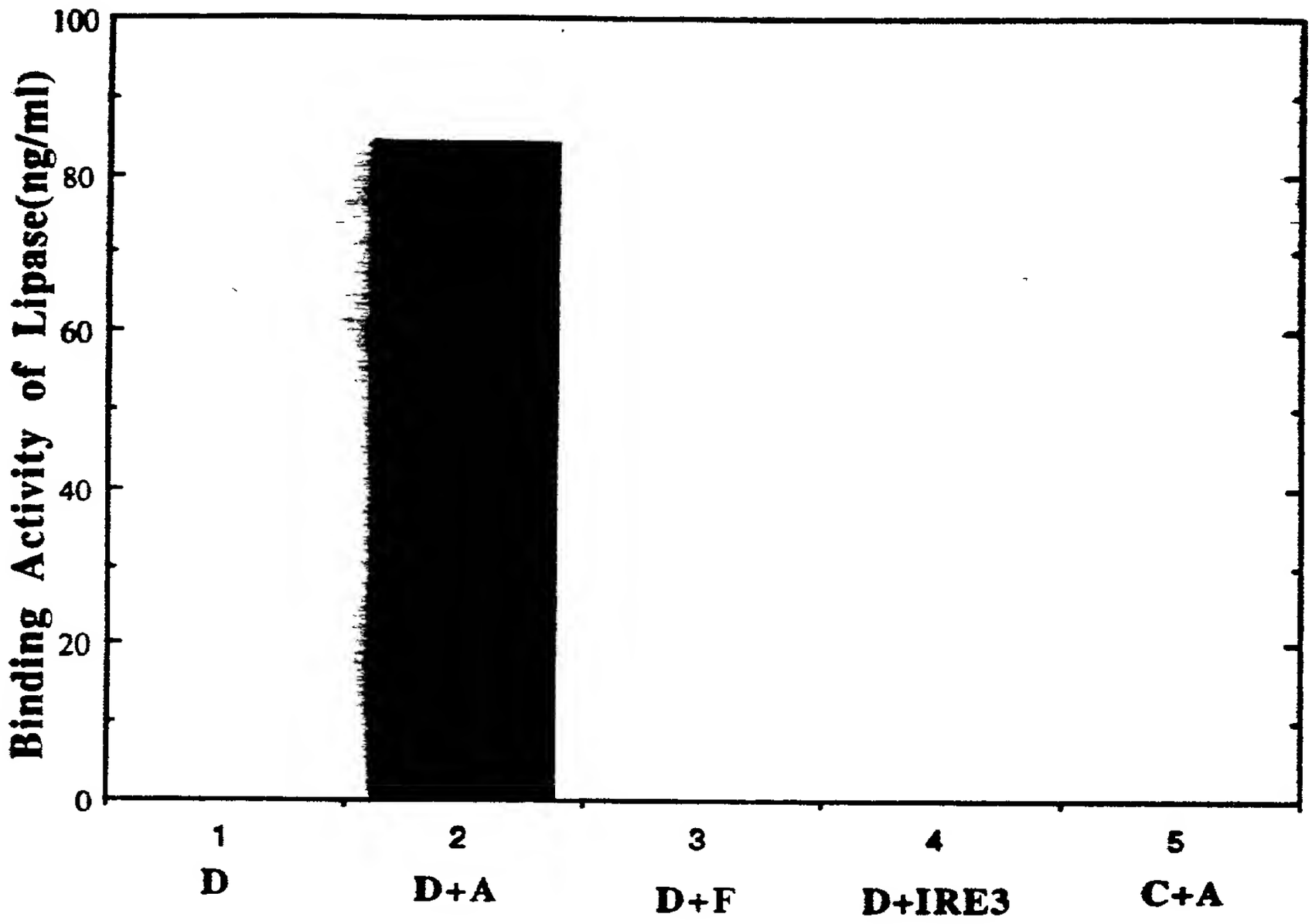

921
986
Factor Xa
Ile Glu Gly Arg ↓Gly Ile Pro Arg Asn Ser Arg Val Asp Ser Ser Gly Arg Ile Val Thr Asp
ATC GAA GGT CGT GGG ATC CCC AGG AAT TCC CGG GTC GAC TCG AGC GGC CGC ATC GTG ACT GAC TGA
BamH I
EcoR I
Sma I
Sal I
Xho I
Not I
Stop codons
Tth111 I (1141)
Aat II (1246)
Bal I (463)
glutathione S-transferase
Ptac
BspM I (63)
pSj10ΔBam7Stop7
Amp
Pst I (1923)
pGEX-5X-3
4974 bp
p4.5
Aiwn I (2643)
Nar I (4312)
Hpa I (4177)
EcoR V (4121)
lacIq
BssH II (4084)
Apa I (3880)
BstE II (3854)
Mlu I (3673)
pBR322 ori

**FIGURE 4**




A—IRE1 + IRE 2 + CBD (10μg/ml)
F—IRE1 + IRE 2 + 60% CBD(10μg/ml)
IRE3 (10μg/ml)
D—Lip-celD (10μg/ml)
C—Lip-Con (10μg/ml)

**FIGURE 5**

Amino Acid sequence of first two internal repeats and CBC of Scaffoldin

Gly-Val-Pro-Ser-Lys-Gly-Met-Ala-Asn-Cys-Asp-Phe-Val-Leu-Gly-Tyr-Asp-Pro-Asn-Val-Leu-Glu-Val-Thr-Glu-Val-Lys-Pro-Gly-Ser-Ile-Ile-Lys-Asp-Pro-Asp-Pro-Ser-Lys-Ser-Phe-Asp-Ser-Ala-Ile-Tyr-Pro-Asp-Arg-Lys-Met-Ile-Val-Phe-Leu-Phe-Ala-Glu-Asp-Ser-Gly-Arg-Gly-Thr-Tyr-Ala-Ile-Thr-Gln-Asp-Gly-Val-Phe-Ala-Thr-Ile-Val-Ala-Thr-Val-Lys-Ser-Ala-Ala-Ala-Ala-Pro-Ile-Thr-Leu-Leu-Glu-Val-Gly-Ala-Phe-Ala-Asp-Asn-Asp-Leu-Val-Glu-Ile-Ser-Thr-Thr-Phe-Val-Ala-Gly-Gly-Val-Asn-Leu-Gly-Ser-Ser-Val-Pro-Thr-Thr-Gln-Pro-Asn-Val-Pro-Ser-Asp-Gly-Val-Val-Val-Glu-Ile-Gly-Lys-Val-Thr-Gly-Ser-Val-Gly-Thr-Thr-Val-Glu-Ile-Pro-Val-Tyr-Phe-Arg-Gly-Val-Pro-Ser-Lys-Gly-Ile-Ala-Asn-Cys-Asp-Phe-Val-Phe-Arg-Tyr-Asp-Pro-Asn-Val-Leu-Glu-Ile-Ile-Gly-Ile-Asp-Pro-Gly-Asp-Ile-Ile-Val-Asp-Pro-Asn-Pro-Thr-Lys-Ser-Phe-Asp-Thr-Ala-Ile-Tyr-Pro-Asp-Arg-Lys-Ile-Ile-Val-Phe-Leu-Phe-Ala-Glu-Asp-Ser-Gly-Thr-Gly-Ala-Tyr-Ala-Ile-Thr-Lys-Asp-Gly-Val-Phe-Ala-Lys-Ile-Arg-Ala-Thr-Val-Lys-Ser-Ser-Ala-Pro-Gly-Tyr-Ile-Thr-Phe-Asp-Glu-Val-Gly-Gly-Phe-Ala-Asp-Asn-Asp-Leu-Val-Glu-Gln-Lys-Val-Ser-Phe-Ile-Asp-Gly-Gly-Val-Asn-Val-Gly-Asn-Ala-Thr-Pro-Thr-Lys-Gly-Ala-Thr-Pro-Thr-Asn-Thr-Ala-Thr-Pro-Thr-Lys-Ser-Ala-Thr-Ala-Thr-Pro-Thr-Arg-Pro-Ser-Val-Pro-Thr-Asn-Thr-Pro-Thr-Asn-Thr-Pro-Ala-Asn-Thr-Pro-Val-Ser-Gly-Asn-Leu-Lys-Val-Glu-Phe-Tyr-Asn-Ser-Asn-Pro-Ser-Asp-Thr-Thr-Asn-Ser-Ile-Asn-Pro-Gln-Phe-Lys-Val-Thr-Asn-Thr-Gly-Ser-Ser-Ala-Ile-Asp-Leu-Ser-Lys-Leu-Thr-Leu-Arg-Tyr-Tyr-Tyr-Thr-Val-Asp-Gly-Gln-Lys-Asp-Gln-Thr-Phe-Trp-Cys-Asp-His-Ala-Ala-Ile-Ile-Gly-Ser-Asn-Gly-Ser-Tyr-Asn-Gly-Ile-Thr-Ser-Asn-Val-Lys-Gly-Thr-Phe-Val-Lys-Met-Ser-Ser-Ser-Thr-Asn-Asn-Ala-Asp-Thr-Tyr-Leu-Glu-Ile-Ser-Phe-Thr-Gly-Gly-Thr-Leu-Glu-Pro-Gly-Ala-His-Val-Gln-Ile-Gln-Gly-Arg-Phe-Ala-Lys-Asn-Asp-Trp-Ser-Asn-Tyr-Thr-Gln-Ser-Asn-Asp-Tyr-Ser-Phe-Lys-Ser-Ala-Ser-Gln-Phe-Val-Glu-Trp-Asp-Gln-Val-Thr-Ala-Tyr-Leu-Asn-Gly-Val-Leu-Val-Trp-Gly-Lys-Glu-Pro-Gly-Gly-Ser-Val-Val-Pro-Ser-Thr-Gln-Pro-Val-Thr-Thr-Pro-Pro-Ala-Thr-Thr-Lys-Pro-Pro-Ala-Thr-Thr-Lys-Pro-Pro-Ala-Thr-Thr-Ile-Pro-Pro-Ser-Asp-Asp-Pro-Asn-Ala-Ile-Lys-Ile-Lys-Val-Asp-Thr-Val-Asn-Ala-Lys-Pro-Gly-Asp-Thr-Val-Asn-Ile-Pro-Val-Arg-Phe-Ser

**FIGURE 6**